

Whole genome fine map of rice completed

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Rice is a staple crop for more than half of the world's population, and it was hoped that the availability of its genome sequence might enable scientists to develop more productive and environment friendly rice strains. Furthermore, the rice genome might provide the key to understanding the genetics of other major cereal crops, as all of them have much larger genomes.

After the completion of a draft sequence of the Chinese hybrid rice genome, which was published in the Journal Science in 2002, CAS researchers have recently finished the fine map of the rice genome. In an article published by the recent issue of PLoS Biology (Vol.3 Issue 2, 2005), scientists led by the Beijing Institute of Genomics (BIG) reported a "much improved, near-complete genome analysis of the indica and japonica subspecies of *O. sativa*."

The fine maps of the rice genome sequences will lay a solid foundation for studying the differences among strains of rice and shed insight into mechanisms of hybrid advantages at a new level, according to BIG researchers.

The efficiency and data quality of the fine maps of two strains of rice, Indica and Japonica, are better than the draft sequence published in 2002. The fine maps were assembled with whole genome shotgun approach. Through searches of 19079 full length cDNA, 97.7% of complete genes were found in the two genomes. After adjusting for residual errors of predictions with EST data, the number of genes is estimated to be between 30,000 to 40,000. Among them, only 2-3% genes are unique to any one of the two strains.

Even though the genetic difference between the two strains is small, there are large differences in intergenic regions. The study also analyzed the duplication history of the rice genome. Eighteen pairs of apparent duplications were discovered, covering 65.7% of the genome. Among them, 17 pairs happened before the divergence of the grasses from other flowering plants. More importantly, the on-going duplications of single genes provided a unlimited source of raw materials for gene genesis, creating differences among the grass family.

The Chinese Superhybrid Rice Genome Project, initiated by BGI in 2000, focused on the hybrid rice "Liang You Pei Jiu" as the basic research object. The hybrid was developed by the famous rice expert Yuan Longping. The goal of the project was to reveal the molecular mechanism of the hybridization advantages, thus providing the theoretical basis for improving output and selecting better strains of agriculture crops. The current publication provided a completed fine map for the paternal strain; °93-11;± (Indica), and its comparison with the genome sequence of the Japonica.

It is reported that BGI will finish whole genome assembly and analysis for the maternal strain "PeiAi 64" (its main genetic background being Japonica, as well as a mixture of Indica and Japonica genes). This would further help discovering distribution of the hybrid genes in F1 and the changes of physiological traits, thus revealing the source of the hybridization advantage in hybrid rice.

Source: CAS

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